

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Aug 03 18:17:33 EDT 2007

=====

Application No: 10597914

Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-03 17:21:53.537

Finished: 2007-08-03 17:21:55.691

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 154 ms

Total Warnings: 54

Total Errors: 0

No. of SeqIDs Defined: 106

Actual SeqID Count: 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
W 213	Artificial or Unknown found in <213> in SEQ ID (56)
W 213	Artificial or Unknown found in <213> in SEQ ID (57)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 213	Artificial or Unknown found in <213> in SEQ ID (69)
W 213	Artificial or Unknown found in <213> in SEQ ID (70)
W 213	Artificial or Unknown found in <213> in SEQ ID (71)
W 213	Artificial or Unknown found in <213> in SEQ ID (72)

**Input Set:**

**Output Set:**

**Started:** 2007-08-03 17:21:53.537  
**Finished:** 2007-08-03 17:21:55.691  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 154 ms  
**Total Warnings:** 54  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> Representative: Greenlee, Winner and Sullivan, P.C.  
HODGES, Robert S  
TRIPET, Brian

<120> COMPOSITIONS AND METHODS FOR MODIFICATION AND PREVENTION OF SARS  
CORONAVIRUS INFECTIVITY

<130> 6-04 WO

<140> 10597914

<141> 2007-08-03

<150> PCT (not assigned)

<151> 2005-02-14

<150> US 60/544,410

<151> 2004-02-12

<160> 106

<170> PatentIn version 3.3

<210> 1

<211> 3768

<212> DNA

<213> SARS coronavirus Urbani

<220>

<221> CDS

<222> (1)..(3768)

<400> 1

atg ttt att ttc tta tta ttt ctt act ctc act agt ggt agt gac ctt	48
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu	
1 5 10 15	
gac cgg tgc acc act ttt gat gat gtt caa gct cct aat tac act caa	96
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln	
20 25 30	
cat act tca tct atg agg ggg gtt tac tat cct gat gaa att ttt aga	144
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg	
35 40 45	
tca gac act ctt tat tta act cag gat tta ttt ctt cca ttt tat tct	192
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser	
50 55 60	
aat gtt aca ggg ttt cat act att aat cat acg ttt ggc aac cct gtc	240
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val	
65 70 75 80	
ata cct ttt aag gat ggt att tat ttt gct gcc aca gag aaa tca aat	288
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn	

85	90	95	
gtt gtc cgt ggt tgg gtt ttt ggt tct acc atg aac aac aag tca cag			336
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln			
100	105	110	
tcg gtg att att att aac aat tct act aat gtt gtt ata cga gca tgt			384
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys			
115	120	125	
aac ttt gaa ttg tgt gac aac cct ttc ttt gct gtt tct aaa ccc atg			432
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met			
130	135	140	
ggg aca cag aca cat act atg ata ttc gat aat gca ttt aat tgc act			480
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr			
145	150	155	160
ttc gag tac ata tct gat gcc ttt tcg ctt gat gtt tca gaa aag tca			528
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser			
165	170	175	
ggg aat ttt aaa cac tta cga gag ttt gtg ttt aaa aat aaa gat ggg			576
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly			
180	185	190	
ttt ctc tat gtt tat aag ggc tat caa cct ata gat gta gtt cgt gat			624
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp			
195	200	205	
cta cct tct ggt ttt aac act ttg aaa cct att ttt aag ttg cct ctt			672
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu			
210	215	220	
ggg att aac att aca aat ttt aga gcc att ctt aca gcc ttt tca cct			720
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro			
225	230	235	240
gct caa gac att tgg ggc acg tca gct gca gcc tat ttt gtt ggc tat			768
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr			
245	250	255	
tta aag cca act aca ttt atg ctc aag tat gat gaa aat ggt aca atc			816
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile			
260	265	270	
aca gat gct gtt gat tgt tct caa aat cca ctt gct gaa ctc aaa tgc			864
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys			
275	280	285	
tct gtt aag agc ttt gag att gac aaa gga att tac cag acc tct aat			912
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn			
290	295	300	
ttc agg gtt gtt ccc tca gga gat gtt gtg aga ttc cct aat att aca			960
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr			
305	310	315	320

aac ttg tgt cct ttt gga gag gtt ttt aat gct act aaa ttc cct tct	1008
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser	
325 330 335	
gtc tat gca tgg gag aga aaa aaa att tct aat tgt gtt gct gat tac	1056
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr	
340 345 350	
tct gtg ctc tac aac tca aca ttt ttt tca acc ttt aag tgc tat ggc	1104
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly	
355 360 365	
gtt tct gcc act aag ttg aat gat ctt tgc ttc tcc aat gtc tat gca	1152
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala	
370 375 380	
gat tct ttt gta gtc aag gga gat gat gta aga caa ata gcg cca gga	1200
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly	
385 390 395 400	
caa act ggt gtt att gct gat tat aat tat aaa ttg cca gat gat ttc	1248
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe	
405 410 415	
atg ggt tgt gtc ctt gct tgg aat act agg aac att gat gct act tca	1296
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser	
420 425 430	
act ggt aat tat aat tat aaa tat agg tat ctt aga cat ggc aag ctt	1344
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu	
435 440 445	
agg ccc ttt gag aga gac ata tct aat gtg cct ttc tcc cct gat ggc	1392
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly	
450 455 460	
aaa cct tgc acc cca cct gct ctt aat tgt tat tgg cca tta aat gat	1440
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp	
465 470 475 480	
tat ggt ttt tac acc act act ggc att ggc tac caa cct tac aga gtt	1488
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val	
485 490 495	
gta gta ctt tct ttt gaa ctt tta aat gca ccg gcc acg gtt tgt gga	1536
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly	
500 505 510	
cca aaa tta tcc act gac ctt att aag aac cag tgt gtc aat ttt aat	1584
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn	
515 520 525	
ttt aat gga ctc act ggt act ggt gtg tta act cct tct tca aag aga	1632
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg	
530 535 540	

ttt caa cca ttt caa caa ttt ggc cgt gat gtt tct gat ttc act gat	1680
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp	
545 550 555 560	
tcc gtt cga gat cct aaa aca tct gaa ata tta gac att tca cct tgc	1728
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys	
565 570 575	
tct ttt ggg ggt gta agt gta att aca cct gga aca aat gct tca tct	1776
Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser	
580 585 590	
gaa gtt gct gtt cta tat caa gat gtt aac tgc act gat gtt tct aca	1824
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr	
595 600 605	
gca att cat gca gat caa ctc aca cca gct tgg cgc ata tat tct act	1872
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr	
610 615 620	
gga aac aat gta ttc cag act caa gca ggc tgt ctt ata gga gct gag	1920
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu	
625 630 635 640	
cat gtc gac act tct tat gag tgc gac att cct att gga gct ggc att	1968
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile	
645 650 655	
tgt gct agt tac cat aca gtt tct tta tta cgt agt act agc caa aaa	2016
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys	
660 665 670	
tct att gtg gct tat act atg tct tta ggt gct gat agt tca att gct	2064
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala	
675 680 685	
tac tct aat aac acc att gct ata cct act aac ttt tca att agc att	2112
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile	
690 695 700	
act aca gaa gta atg cct gtt tct atg gct aaa acc tcc gta gat tgt	2160
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys	
705 710 715 720	
aat atg tac atc tgc gga gat tct act gaa tgt gct aat ttg ctt ctc	2208
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu	
725 730 735	
caa tat ggt agc ttt tgc aca caa cta aat cgt gca ctc tca ggt att	2256
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile	
740 745 750	
gct gct gaa cag gat cgc aac aca cgt gaa gtg ttc gct caa gtc aaa	2304
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys	
755 760 765	
caa atg tac aaa acc cca act ttg aaa tat ttt ggt ggt ttt aat ttt	2352

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe	
770 775 780	
tca caa ata tta cct gac cct cta aag cca act aag agg tct ttt att	2400
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile	
785 790 795 800	
gag gac ttg ctc ttt aat aag gtg aca ctc gct gat gct ggc ttc atg	2448
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met	
805 810 815	
aag caa tat ggc gaa tgc cta ggt gat att aat gct aga gat ctc att	2496
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile	
820 825 830	
tgt gcg cag aag ttc aat gga ctt aca gtg ttg cca cct ctg ctc act	2544
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr	
835 840 845	
gat gat atg att gct gcc tac act gct gct cta gtt agt ggt act gcc	2592
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala	
850 855 860	
act gct gga tgg aca ttt ggt gct ggc gct gct ctt caa ata cct ttt	2640
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe	
865 870 875 880	
gct atg caa atg gca tat agg ttc aat ggc att gga gtt acc caa aat	2688
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn	
885 890 895	
ggt ctc tat gag aac caa aaa caa atc gcc aac caa ttt aac aag gcg	2736
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala	
900 905 910	
att agt caa att caa gaa tca ctt aca aca aca tca act gca ttg ggc	2784
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly	
915 920 925	
aag ctg caa gac gtt gtt aac cag aat gct caa gca tta aac aca ctt	2832
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu	
930 935 940	
ggt aaa caa ctt agc tct aat ttt ggt gca att tca agt gtg cta aat	2880
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn	
945 950 955 960	
gat atc ctt tcg cga ctt gat aaa gtc gag gcg gag gta caa att gac	2928
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp	
965 970 975	
agg tta att aca ggc aga ctt caa agc ctt caa acc tat gta aca caa	2976
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln	
980 985 990	
caa cta atc agg gct gct gaa atc agg gct tct gct aat ctt gct gct	3024
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala	



995						1000						1005						
act	aaa	atg	tct	gag	tgt	gtt	ctt	gga	caa	tca	aaa	aga	gtt	gac	3069			
Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg	Val	Asp				
1010						1015						1020						
ttt	tgt	gga	aag	ggc	tac	cac	ctt	atg	tcc	ttc	cca	caa	gca	gcc	3114			
Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln	Ala	Ala				
1025						1030						1035						
ccg	cat	ggt	gtt	gtc	ttc	cta	cat	gtc	acg	tat	gtg	cca	tcc	cag	3159			
Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro	Ser	Gln				
1040						1045						1050						
gag	agg	aac	ttc	acc	aca	gcg	cca	gca	att	tgt	cat	gaa	ggc	aaa	3204			
Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Glu	Gly	Lys				
1055						1060						1065						
gca	tac	ttc	cct	cgt	gaa	ggg	gtt	ttt	gtg	ttt	aat	ggc	act	tct	3249			
Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	Thr	Ser				
1070						1075						1080						
tgg	ttt	att	aca	cag	agg	aac	ttc	ttt	tct	cca	caa	ata	att	act	3294			
Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	Thr				
1085						1090						1095						
aca	gac	aat	aca	ttt	gtc	tca	gga	aat	tgt	gat	gtc	gtt	att	ggc	3339			
Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly				
1100						1105						1110						
atc	att	aac	aac	aca	gtt	tat	gat	cct	ctg	caa	cct	gag	ctc	gac	3384			
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp				
1115						1120						1125						
tca	ttc	aaa	gaa	gag	ctg	gac	aag	tac	ttc	aaa	aat	cat	aca	tca	3429			
Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser				
1130						1135						1140						
cca	gat	gtt	gat	ctt	ggc	gac	att	tca	ggc	att	aac	gct	tct	gtc	3474			
Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val				
1145						1150						1155						
gtc	aac	att	caa	aaa	gaa	att	gac	cgc	ctc	aat	gag	gtc	gct	aaa	3519			
Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys				
1160						1165						1170						
aat	tta	aat	gaa	tca	ctc	att	gac	ctt	caa	gaa	ttg	gga	aaa	tat	3564			
Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr				
1175						1180						1185						
gag	caa	tat	att	aaa	tgg	cct	tgg	tat	gtt	tgg	ctc	ggc	ttc	att	3609			
Glu	Gln	Tyr	Ile	Lys	Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile				
1190						1195						1200						
gct	gga	cta	att	gcc	atc	gtc	atg	gtt	aca	atc	ttg	ctt	tgt	tgc	3654			
Ala	Gly	Leu	Ile	Ala	Ile	Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys				
1205						1210						1215						

atg act agt tgt tgc agt tgc ctc aag